Microbial co-existence and stable equilibria in a mechanistic model of enteric methane production

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Abstract

Globally, 14.5% of all anthropogenic greenhouse gases come from ruminants. One of these is methane, which is produced in the rumen of ruminant animals. Feed is degraded by microbes to produce volatile fatty acids (which are absorbed by the animal) and hydrogen (which is metabolized by methanogens to form methane). The dynamics of hydrogen production and metabolism are subject to thermodynamic control imposed by the hydrogen concentration. Existing models to estimate methane production are based on calculation of hydrogen balances without considering the presence of methanogens and do not include thermodynamic control. In this project, a model is developed based on glucose-hydrogen-methanogen dynamics to estimate methane production and illustrates a co-existence of microbes that employs different fermentation pathways competing for the same food source in the rumen. Glucose was chosen as an example of a fermentable feed component. A thermodynamic term was integrated into a Monod-type model to represent the thermodynamic control of hydrogen concentration on the rates of hydrogen generation and hydrogen metabolism. Results of this model suggest that the microbial community composition and the combination of the different pathways are determined by the rumen environment, biological parameters of the microbes and the feedback imposed by substrate and product concentrations. The mathematical enunciation of this model is therefore consistent with biological expectations. This model could be expanded to include plant polymer degradation rate, feeding level and feeding frequency to explore their effects on methane production. This model could also be integrated into models of whole rumen function to address more complex questions. It would also support experimentation

with animals for understanding factors that control methane formation and to explore methane mitigation strategies.

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Abbreviations

ADP	Adenosine diphosphate
ATP	Adenosine triphosphate (used by microbes for maintenance and reproduction)
VFA	Volatile fatty acids (e.g., acetate, propionate and butyrate)
HM	Hydrogen-methanogen dynamics
HM^{θ}	Hydrogen-methanogen dynamics with thermodynamic term
GHM^{θ}	Glucose-hydrogen-methanogen dynamics with thermodynamic term

Nomenclature

Subscript

Substrate	Description
h	hydrogen
g	glucose
A	acetate
P	propionate
B	butyrate

Microbe	Description
m	methanogens
i	glucose fermenters

Superscript

Notation	Description
$*$	equilibrium point (steady state solution) of variables

Variables

Notation	Description	Unit
t	time	s
S	substrate concentration	mol ml^{-1}
X	microbe population density	cell ml^{-1}
θ	thermodynamic term	unitless
M	estimated methane production	$rumen^{-1}$ d^{-1}

Parameters

Rumen environment	Description	Unit
α	passage rate through the rumen	s^{-1}
β	rate of substrate generation	mol ml^{-1} s^{-1}
γ	absorption rate of substrate	s^{-1}

Microbe	Description	Unit
q	maximal rate at which a microbe can metabolize substrate	mol $cell^{-1}$ s^{-1}
K	substrate concentration at half of q assuming no thermodynamic feedback	mol ml^{-1}
w	moles of product generated from metabolizing per mole of substrate	unitless
n	ATP gained by microbe from metabolizing per mole of substrate	mol_{ATP} mol^{-1}
m	maintenance requirement of a microbe	mol_{ATP} $cell^{-1}$ s^{-1}
Y	reproduction coefficient of microbe	cell mol_{ATP}^{-1}
μ	reproduction rate of microbe	s^{-1}
d	death coefficient of microbe	s^{-1}

Thermodynamic term	Description	Unit
T	temperature	K
$\mathcal{R}$	ideal gas constant	kJ mol^{-1} K^{-1}
ΔG_T^o	Gibbs free energy of a chemical reaction at T under standard conditions	kJ mol^{-1}
ΔG_{ATP}	energy required to generate one unit of ATP	kJ mol_{ATP}^{-1}